AU 1814

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

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 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:                 ENTERED
 4
 5       (i) APPLICANT: Amgen Inc.
 6
 7
 8
 9      (ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
10
11     (iii) NUMBER OF SEQUENCES: 6
12
13      (iv) CORRESPONDENCE ADDRESS:
14              (A) ADDRESSEE: Amgen Inc.
15              (B) STREET: 1840 Dehavilland Drive
16              (C) CITY: Thousand Oaks
17              (D) STATE: California
18              (E) COUNTRY: U.S.A.
19              (F) ZIP: 91230-1789
20
21       (v) COMPUTER READABLE FORM:
22              (A) MEDIUM TYPE: Floppy disk
23              (B) COMPUTER: IBM PC compatible
24              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27      (vi) CURRENT APPLICATION DATA:
28              (A) APPLICATION NUMBER: US 08/474,833
29              (B) FILING DATE: 07-JUN-1995
30              (C) CLASSIFICATION:
31
32    (viii) ATTORNEY/AGENT INFORMATION:
33              (A) NAME: Pessin, Karol M.
34              (C) REFERENCE/DOCKET NUMBER: A-345
35
36
37   (2) INFORMATION FOR SEQ ID NO:1:
38
39       (i) SEQUENCE CHARACTERISTICS:
40              (A) LENGTH: 491 base pairs
41              (B) TYPE: nucleic acid
42              (C) STRANDEDNESS: double
43              (D) TOPOLOGY: linear
44
45      (ii) MOLECULE TYPE: cDNA
46
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/474,833*

DATE: 05/19/96
TIME: 17:02:10

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47
48
49
50   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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56 CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA   180
57
58 CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC   240
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60 CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT   300
61
62 GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA   360
63
64 ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT   420
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66 GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG   480
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68 TTAATGGATC C   491
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70 (2) INFORMATION FOR SEQ ID NO:2:
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72   (i) SEQUENCE CHARACTERISTICS:
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74   (B) TYPE: nucleic acid
75   (C) STRANDEDNESS: double
76   (D) TOPOLOGY: linear
77
78   (ii) MOLECULE TYPE: cDNA
79
80
81
82
83   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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85 AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA   60
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87 AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAGTCAGT   120
88
89 GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT   180
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91 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG   240
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93 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA   300
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95 CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT   360
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97 TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAACGAGA   420
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99 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC   480

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103    (2) INFORMATION FOR SEQ ID NO:3:
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105        (i) SEQUENCE CHARACTERISTICS:
106            (A) LENGTH: 147 amino acids
107            (B) TYPE: amino acid
108            (C) STRANDEDNESS: single
109            (D) TOPOLOGY: linear
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111       (ii) MOLECULE TYPE: protein
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113
114
115
116       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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118       Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
119       1               5                   10                  15
120
121       Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
122                   20                  25                  30
123
124       Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
125           35                  40                  45
126
127       Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
128           50                  55                  60
129
130       Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
131       65                  70                  75                  80
132
133       Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
134                   85                  90                  95
135
136       Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
137                   100                 105                 110
138
139       Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
140                   115                 120                 125
141
142       Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
143               130                 135                 140
144
145       Pro Glu Cys
146       145
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148    (2) INFORMATION FOR SEQ ID NO:4:
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150        (i) SEQUENCE CHARACTERISTICS:
151            (A) LENGTH: 454 base pairs
152            (B) TYPE: nucleic acid
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153                   (C) STRANDEDNESS: double
154                   (D) TOPOLOGY: linear
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156           (ii) MOLECULE TYPE: cDNA
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161           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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163   CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT      60
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166
167   CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCTG     180
168
169   GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCTTCA GATCTCTAAC     240
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171   GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG     300
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173   CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGGTCCTGGA AGCATCCGGT     360
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175   TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG     420
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177   CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC                                 454
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182                   (A) LENGTH: 454 base pairs
183                   (B) TYPE: nucleic acid
184                   (C) STRANDEDNESS: double
185                   (D) TOPOLOGY: linear
186
187           (ii) MOLECULE TYPE: cDNA
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189
190
191
192           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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194   GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA      60
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196   TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG     120
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198   GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC     180
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200   CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG     240
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202   CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC     300
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204   GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA     360
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206   ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC      420
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208   GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG                                   454
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210   (2) INFORMATION FOR SEQ ID NO:6:
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212        (i) SEQUENCE CHARACTERISTICS:
213             (A) LENGTH: 147 amino acids
214             (B) TYPE: amino acid
215             (C) STRANDEDNESS: single
216             (D) TOPOLOGY: linear
217
218       (ii) MOLECULE TYPE: protein
219
220
221
222
223       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
224
225       Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
226       1               5               10              15
227
228       Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
229                   20              25                  30
230
231       Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
232               35              40              45
233
234       Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
235           50              55              60
236
237       Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
238       65              70              75              80
239
240       Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
241                   85              90              95
242
243       Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
244               100             105             110
245
246       Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
247               115             120             125
248
249       Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
250           130             135             140
251
252       Pro Gly Cys
253       145
254
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/474,833*

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